

Exhibit 3

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQ_184 1433 aa

Sequence 2: G_kaustophilus 1444 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 99

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-22024725.dnd]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:31068

Alignment Score 8866

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-22024725.aln]

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SEQ_184      -----MVTKEQKERFLILLEQLKMTSDEWMPHFREAAIRKVVIDKEEKSWHFYFQ 50
G_kaustophilus MMLRGEQTDVMVTKEQKERFLILLEQLKMTSDEWMPHFREAAIRKVVIDKEEKSWHFYFQ 60
                *****

SEQ_184      FDNVLPVHVYKTFADRLQTAFRHIAAVRHTMEVEAPRVTEADVQAYWPLCLAEQLQEGMSP 110
G_kaustophilus FDNVLPVHVYKTFADRLQTAFRHIAAVRHTMEVEAPRVTEADVQAYWPLCLAEQLQEGMSP 120
                *****

SEQ_184      LVDWLSRQTPPELKGKLLVVARHEAEALAIKRRFAKKIADVYASFGFPPLQLDVSVEPSK 170
G_kaustophilus LVDWLSRQTPPELKGKLLVVARHEAEALAIKRRFAKKIADVYASFGFPPLQLDVSVEPSK 180
                *****

SEQ_184      QEMEQLAQKQEQEDEERALAVLTDLAREEEKAASAPPSGFLVIGYPIRDEEPPVRRLETIV 230
G_kaustophilus QEMEQLAQKQEQEDEERALAVLTDLAREEEKAASAPPSGFLVIGYPIRDEEPPVRRLETIV 240
                *****

SEQ_184      EEERRVVVQGYVFDAEVSELKSGRTLLTMKITDYTNSILVKMFSDRKEDAELMSGVKKGM 290
G_kaustophilus EEERRVVVQGYVFDAEVSELKSGRTLLTMKITDYTNSILVKMFSDRKEDAELMSGVKKGM 300
                *****

SEQ_184      WVKVRGSVQNDTFVRDLVIIANDLNEIAANERQDTAPEGEKRVELHLHTPMSQMDAVTSV 350
G_kaustophilus WVKVRGSVQNDTFVRDLVIIANDLNEIAANERQDTAPEGEKRVELHLHTPMSQMDAVTSV 360
                *****

SEQ_184      TKLIEQAKKWGHPAIAVTDHAVVQSEFPEAYSAAKKHGMKVIYGLEANIVDDGVPIAYNET 410
G_kaustophilus TKLIEQAKKWGHPAIAVTDHAVVQSEFPEAYSAAKKHGMKVIYGLEANIVDDGVPIAYNET 420
                *****

SEQ_184      HRRLESEETYVVFDEVTTGLSAVYNTIIELAAVKVVDGEIIDRFMSFANPGHPLSVTTMEL 470
G_kaustophilus HRRLESEETYVVFDEVTTGLSAVYNTIIELAAVKVVDGEIIDRFMSFANPGHPLSVTTMEL 480
                *****

SEQ_184      TGITDEMVKDAPKPDDEVLARFVDWAGDATLVAHNASFDIGFLNAGLARMGRGKIANPVID 530
G_kaustophilus TGITDEMVKDAPKPDDEVLARFVDWAGDATLVAHNASFDIGFLNTGLARMGRGKIANPVID 540
                *****;*****

SEQ_184      TLELARFLYPDLKNHRLNTLCKKFDIELTQHHRAIYDAEATGHLLMRLLKEAEERGILFH 590
G_kaustophilus TLELARFLYPDLKNHRLNTLCKKFDIELTQHHRAIYDAEATGHLLMRLLKEAEERGILFH 600
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SEQ_184	DELNSRTHSEASYRLARPFHVTLQAQNETGLKNLFKLVSLSHIQYFHRVPRIPRSVLVKH	650
G_kaustophilus	DELNSRTHSEASYRLARPFHVTLQAQNETGLKNLFKLVSLSHIQYFHRVPRIPRSVLVKH	660

SEQ_184	RDGLLVGSGCDKGELFDNLIQKAPEEVEDIARFYDFLEVHPPDVYKPLIEMDYVKDEEMI	710
G_kaustophilus	RDGLLVGSGCDKGELFDNLIQKAPEEVEDIARFYDFLEVHPPDVYKPLIEMDYVKDEEMI	720

SEQ_184	KNIIRSIVALGEKLDIPVVATGNVHYLNPEDKIYRKILIHSSQGGANPLNRHELDPDVFRT	770
G_kaustophilus	KNIIRSIVALGEKLDIPVVATGNVHYLNPEDKIYRKILIHSSQGGANPLNRHELDPDVFRT	780

SEQ_184	TNEMLDCFSFLGPEKAKEIVVDNTQKIASLIGDVKPIKDELYTPRIEGADEEIREMSYRR	830
G_kaustophilus	TNEMLDCFSFLGPEKAKEIVVDNTQKIASLIGDVKPIKDELYTPRIEGADEEIREMSYRR	840

SEQ_184	AKEIYGDPLPKLVEERLEKELKSIIGHGFAVIYLI SHKLVKKS LDDGYLVGSRG SVGSSF	890
G_kaustophilus	AKEIYGDPLPKLVEERLEKELKSIIGHGFAVIYLI SHKLVKKS LDDGYLVGSRG SVGSSF	900

SEQ_184	VATMTEITEVNPLPPHYVCPNCKHSEFFNDGSGVSGGFDLPDKNCPRCGTYKKDGHDI PF	950
G_kaustophilus	VATMTEITEVNPLPPHYVCPNCKHSEFFNDGSGVSGGFDLPDKNCPRCGTYKKDGHDI PF	960

SEQ_184	ETFLGFKGDKVPDIDLNFSGEYQ PRAHNYTKVLF GEDNVYRAGTIGTVADKTAYGFVKAY	1010
G_kaustophilus	ETFLGFKGDKVPDIDLNFSGEYQ PRAHNYTKVLF GEDNVYRAGTIGTVADKTAYGFVKAY	1020

SEQ_184	ASDHNLELRGA EID-LAAGCTGVKRTTGQHPGGIIVVPDYMEIYDFTPIQYPADDT SSEW	1069
G_kaustophilus	ASDHNLELRGA EIDRLAAGCTGVKRTTGQHPGGIIVVPDYMEIYDFTPIQYPADDT SSEW	1080

SEQ_184	RTTHFD FHSIHDNLLKLDILGHDDPTVIRMLQDL SGIDPKTIPTDDPDVMGIF SSTEPLG	1129
G_kaustophilus	RTTHFD FHSIHDNLLKLDILGHDDPTVIRMLQDL SGIDPKTIPTDDPDVMGIF SSTEPLG	1140

SEQ_184	VTPEQIMCNVGTIGIPEFGTRFVRQMLEETRPKTFSELVQISGLSHGTDVWLGN AQELIQ	1189
G_kaustophilus	VTPEQIMCNVGTIGIPEFGTRFVRQMLEETRPKTFSELVQISGLSHGTDVWLGN AQELIQ	1200

SEQ_184	NGTCTLSEVIGCRDDIMVYLIYRGLEPSLAFKIMESVRKGKGLTPEFEAEMRKHDVPEWY	1249
G_kaustophilus	NGTCTLSEVIGCRDDIMVYLIYRGLEPSLAFKIMESVRKGKGLTPEFEAEMRKHDVPEWY	1260

SEQ_184	IDSCKKIKYMF PKAHAAAYVLM AVRIAYFKVHHPLLYYASYFTVRAEDFDLDAMIKGSPA	1309
G_kaustophilus	IDSCKKIKYMF PKAHAAAYVLM AVRIAYFKVHHPLLYYASYFTVRAEDFDLDAMIKGSAA	1320

SEQ_184	IRKRIEEINAKGIQATAKEKSLT VLEVALEMCERGFSFKNIDLYRSQATEFVIDGNSLI	1369
G_kaustophilus	IRKRIEEINAKGIQATAKEKSLT VLEVALEMCERGFSFKNIDLYRSQATEFVIDGNSLI	1380

SEQ_184	PPFNAIPGLGTNVAQAIVRAREEGEFLSKEDLQQRGKLSKTLLEYLESRGCLDSL PDHNQ	1429
G_kaustophilus	PPFNAIPGLGTNVAQAIVRAREEGEFLSKEDLQQRGKLSKTLLEYLESRGCLDSL PDHNQ	1440

SEQ_184	LSLF	1433
G_kaustophilus	LSLF	1444
